CLAIMS

What is claimed is:

1. A method for synthesizing a peptide based on matching a physicochemical

5   mode of a peptide to the same physicochemical mode of a target polypeptide or protein,

followed by synthesizing a retro-inverso peptide version of said peptide comprised of D-

amino acids, comprising the steps of:

assigning a numerical value of an orderable physicochemical property to each

member of a set of peptide constituents, said set of peptide constituents including all the

10   members of the set of naturally-occurring L-amino acids;

arranging said peptide constituents in order of said numerical values of said

orderable physicochemical property;

partitioning said set of peptide constituents into a plurality of peptide constituent

groups, whereby each of said peptide constituent groups contains at least one member of

15   said set of peptide constituents, each peptide constituent group encompasses a range of

said ordered numerical values, and each member of said set of peptide constituents

belongs to only one peptide constitutent group;

creating a polypeptide physicochemical data series by replacing each amino acid

in an amino acid sequence of said target polypeptide or protein with said numerical value

20   of said orderable physicochemical property corresponding to said each amino acid in said

amino acid sequence of said target polypeptide or protein;

calculating one or more polypeptide eigenvalues and a corresponding polypeptide

eigenvector associated with each of said one or more polypeptide eigenvalues by linear

decomposition of an autocovariance matrix formed from a sequentially lagged data

matrix of said polypeptide physicochemical data series;

ordering said one or more polypeptide eigenvalues and said corresponding

polypeptide eigenvectors from largest to smallest;

5   selecting one or more of said polypeptide eigenvectors;

transforming said one or more of said polypeptide eigenvectors into an

eigenvector template;

forming a graph of said eigenvector template, wherein said numerical values of

said physicochemical property are graphed along the y-axis of said graph and ordered

10   position in said eigenvector template is graphed along the x-axis of said graph;

partitioning said graph along said y-axis according to said ranges of said

numerical values of said physicochemical property defining said peptide constituent

groups, to form a plurality of y-axis ranges;

assigning one of said peptide constituents to each position in said peptide by using

15   said graph as a template to create a sequence of a mode-matched peptide, wherein at each

ordered position in said eigenvector template along said x-axis of said graph, said one of

said peptide constituents assigned to said ordered position has a value of said orderable

physicochemical property that is within said y-axis range of said ordered point;

determining a sequence of a retro-inverso peptide by inverting said sequence of a

20   mode-matched peptide; and

synthesizing said retro-inverso peptide from said sequence, using D-amino acids.

2. A method for synthesizing a peptide based on matching a physicochemical mode of a peptide to the same physicochemical mode of a target polypeptide or protein, followed by synthesizing a retro-inverso version of said peptide comprised of D-amino acids, comprising the steps of:

5   assigning a numerical value of an orderable physicochemical property to each member of a set of peptide constituents, said set of peptide constituents including all the members of the set of naturally-occurring amino acids;

     arranging said peptide constituents in order of said numerical values of said orderable physicochemical property;

10   partitioning said set of peptide constituents into a plurality of peptide constituent groups, whereby each of said peptide constituent groups contains at least one member of said set of peptide constituents, each peptide constituent group encompasses a range of said ordered numerical values, and each member of said set of peptide constituents belongs to only one peptide constituent group;

15   creating a polypeptide physicochemical data series by replacing each amino acid in an amino acid sequence with said numerical value of said orderable physicochemical property corresponding to said each amino acid in said amino acid sequence;

     calculating one or more polypeptide eigenvalues and a corresponding polypeptide eigenvector associated with each of said one or more polypeptide eigenvalues by linear

20   decomposition of an autocovariance matrix formed from a sequentially lagged data matrix of said polypeptide physicochemical data series;

     ordering said one or more polypeptide eigenvalues and said corresponding polypeptide eigenvectors from largest to smallest;

selecting one or more of said polypeptide eigenvectors;

forming a vector, said vector being a sum of the products of each of said plurality of said polypeptide eigenvectors multiplied by the corresponding eigenvalue;

forming a graph of said vector, wherein said numerical values of said orderable

5   physicochemical property are graphed along the y-axis of said graph, and ordered

position in said eigenvector template is graphed along the x-axis of said graph;

partitioning said graph along said y-axis according to said range of said numerical values of said orderable physicochemical property defining said peptide constituent groups, to form a plurality of y-axis ranges; and

10   assigning one of said peptide constituents to each position in said peptide by using said graph of said vector as a template, wherein at each ordered position in said eigenvector template along said x-axis of said graph, said one of said peptide constituents assigned to said ordered position has a value of said orderable physicochemical property that is within said y-axis range of said ordered position;

15   determining a sequence of a retro-inverso peptide by inverting said sequence of a mode-matched peptide; and

synthesizing said retro-inverso peptide from said sequence, using D-amino acids.